

RAW SEQUENCE LISTING

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Application Serial Number: 10/619,992 A
Source: IFW16
Date Processed by STIC: 12/06/2005

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IFW16

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DATE: 12/06/2005

PATENT APPLICATION: US/10/619,992A

TIME: 13:09:50

Input Set : D:\00-617-F.ST25.txt

Output Set: N:\CRF4\12062005\J619992A.raw

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3 <110> APPLICANT: Oregon Health & Science University
4       Hefeneider, Steven
5       Bennett, Robert
6       Seiss, Donald
7       Merkins, Louise
9 <120> TITLE OF INVENTION: Mammalian Cell Surface DNA Receptor
11 <130> FILE REFERENCE: 00-617-F
13 <140> CURRENT APPLICATION NUMBER: US 10/619992A
14 <141> CURRENT FILING DATE: 2003-07-15
16 <150> PRIOR APPLICATION NUMBER: 09/921,099
17 <151> PRIOR FILING DATE: 2001-08-01
19 <160> NUMBER OF SEQ ID NOS: 21
21 <170> SOFTWARE: PatentIn version 3.3
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 4351
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (602)..(4174)
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38 tattatgttt tggggtagct gttatccaag ggaaacactt ttttaaacaa caaaacaaaa      180
40 aaaccgcccc gcagtcacaa gtaatttggt ttcctaaaaa tggaatatgg aaagttaatt      240
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44 caaccaatat aaatacagtt tagttgaaag gaacactatt aaggatttgt ttccaggcag      360
46 aatttcagaa atgtaattaa ttcagcaaat aggtttttta aaaaagacat ccaaaggtta      420
48 taaaattatt tagaagtatt ttaggtctga agctgtaata gttgacttaa gcaattaact      480
50 cttcaaaggt gaatgatgaa tatgtgggta attcatactt ttgtccattt ctagcttaca      540
52 aaacactaca cagcaaaata atgatctgct agactgctaa cccgagcatc cagcttccac      600
54 a atg cct gtg cag gca gct caa tgg aca gaa ttt ctg tcc tgt cca atc      649
55 Met Pro Val Gln Ala Ala Gln Trp Thr Glu Phe Leu Ser Cys Pro Ile
56 1           5           10           15
58 tgc tat aat gaa ttt gat gag aat gtg cac aaa ccc atc agt tta ggt      697
59 Cys Tyr Asn Glu Phe Asp Glu Asn Val His Lys Pro Ile Ser Leu Gly
60           20           25           30
62 tgt tca cac act gtt tgc aag acc tgc ttg aat aaa ctt cat cga aaa      745
63 Cys Ser His Thr Val Cys Lys Thr Cys Leu Asn Lys Leu His Arg Lys
64           35           40           45
66 gct tgt cct ttt gac cag act gcc atc aac aca gat att gat gta ctt      793
67 Ala Cys Pro Phe Asp Gln Thr Ala Ile Asn Thr Asp Ile Asp Val Leu
68           50           55           60

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72	65 70 75 80	
74	cat cag tca att aag tta agt aat cta ggt gag aat aaa cac tat gag	889
75	His Gln Ser Ile Lys Leu Ser Asn Leu Gly Glu Asn Lys His Tyr Glu	
76	85 90 95	
78	gtt gca aag aaa tgc gtt gag gat ttg gca ctc tac tta aaa cca cta	937
79	Val Ala Lys Lys Cys Val Glu Asp Leu Ala Leu Tyr Leu Lys Pro Leu	
80	100 105 110	
82	agt gga ggt aaa ggt gta gct agc ttg aac cag agt gca ctg agc cgt	985
83	Ser Gly Gly Lys Gly Val Ala Ser Leu Asn Gln Ser Ala Leu Ser Arg	
84	115 120 125	
86	cca atg caa agg aaa ctg gtg aca ctt gta aac tgt caa ctg gtg gag	1033
87	Pro Met Gln Arg Lys Leu Val Thr Leu Val Asn Cys Gln Leu Val Glu	
88	130 135 140	
90	gaa gaa ggt cgt gta aga gcc atg cga gca gct cgt tcc ctt gga gaa	1081
91	Glu Glu Gly Arg Val Arg Ala Met Arg Ala Ala Arg Ser Leu Gly Glu	
92	145 150 155 160	
94	aga act gta aca gaa ctg ata tta cag cac cag aac cct cag cag ttg	1129
95	Arg Thr Val Thr Glu Leu Ile Leu Gln His Gln Asn Pro Gln Gln Leu	
96	165 170 175	
98	tct gcc aat cta tgg gcc gct gtc agg gct cga gga tgc cag ttt tta	1177
99	Ser Ala Asn Leu Trp Ala Ala Val Arg Ala Arg Gly Cys Gln Phe Leu	
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102	ggg cca gct atg caa gaa gag gcc ttg aag ctg gtg tta ctg gca tta	1225
103	Gly Pro Ala Met Gln Glu Glu Ala Leu Lys Leu Val Leu Leu Ala Leu	
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106	gaa gat ggt tct gcc ctc tca agg aaa gtt ctg gta ctt ttt gtt gtg	1273
107	Glu Asp Gly Ser Ala Leu Ser Arg Lys Val Leu Val Leu Phe Val Val	
108	210 215 220	
110	cag aga cta gaa cca aga ttt cct cag gca tca aaa aca agt att ggt	1321
111	Gln Arg Leu Glu Pro Arg Phe Pro Gln Ala Ser Lys Thr Ser Ile Gly	
112	225 230 235 240	
114	cat gtt gtg caa cta ctg tat cga gct tct tgt ttt aag gtt acc aaa	1369
115	His Val Val Gln Leu Leu Tyr Arg Ala Ser Cys Phe Lys Val Thr Lys	
116	245 250 255	
118	aga gat gaa gac tct tcc cta atg cag ctg aag gag gaa ttt cgg agt	1417
119	Arg Asp Glu Asp Ser Ser Leu Met Gln Leu Lys Glu Glu Phe Arg Ser	
120	260 265 270	
122	tat gaa gca tta cgc aga gaa cat gat gcc caa att gtt cat att gcc	1465
123	Tyr Glu Ala Leu Arg Arg Glu His Asp Ala Gln Ile Val His Ile Ala	
124	275 280 285	
126	atg gaa gca gga ctc cgt att tca cct gaa cag tgg tcc tct ctt ttg	1513
127	Met Glu Ala Gly Leu Arg Ile Ser Pro Glu Gln Trp Ser Ser Leu Leu	
128	290 295 300	
130	tat ggt gat ttg gct cat aaa tca cac atg cag tct atc att gat aag	1561
131	Tyr Gly Asp Leu Ala His Lys Ser His Met Gln Ser Ile Ile Asp Lys	
132	305 310 315 320	
134	cta cag tct cca gag tca ttt gca aag agt gtc cag gaa ttg aca att	1609

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139	Val	Leu	Gln	Arg	Thr	Gly	Asp	Pro	Ala	Asn	Leu	Asn	Arg	Leu	Arg	Pro	
140				340					345					350			
142	cat	tta	gag	ctt	ctt	gca	aac	ata	gac	cct	aat	cca	gac	gct	gtt	tca	1705
143	His	Leu	Glu	Leu	Leu	Ala	Asn	Ile	Asp	Pro	Asn	Pro	Asp	Ala	Val	Ser	
144			355				360						365				
146	cca	act	tgg	gag	cag	ctg	gaa	aat	gca	atg	gta	gct	gtt	aaa	aca	gta	1753
147	Pro	Thr	Trp	Glu	Gln	Leu	Glu	Asn	Ala	Met	Val	Ala	Val	Lys	Thr	Val	
148		370					375					380					
150	gtt	cat	ggc	ctt	gtg	gac	ttc	ata	caa	aat	tat	agt	aga	aaa	ggc	cat	1801
151	Val	His	Gly	Leu	Val	Asp	Phe	Ile	Gln	Asn	Tyr	Ser	Arg	Lys	Gly	His	
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155	Glu	Thr	Pro	Gln	Pro	Gln	Pro	Asn	Ser	Lys	Tyr	Lys	Thr	Ser	Met	Cys	
156				405					410					415			
158	cga	gat	ttg	cga	cag	cag	ggg	ggt	tgt	cca	cga	gga	aca	aat	tgt	aca	1897
159	Arg	Asp	Leu	Arg	Gln	Gln	Gly	Gly	Cys	Pro	Arg	Gly	Thr	Asn	Cys	Thr	
160			420					425					430				
162	ttt	gcc	cat	tct	cag	gaa	gag	ctt	gaa	aag	tat	cga	tta	agg	aac	aaa	1945
163	Phe	Ala	His	Ser	Gln	Glu	Glu	Leu	Glu	Lys	Tyr	Arg	Leu	Arg	Asn	Lys	
164			435				440						445				
166	aag	atc	aat	gcc	act	gta	aga	acg	ttt	cct	ctt	cta	aat	aaa	gtt	ggt	1993
167	Lys	Ile	Asn	Ala	Thr	Val	Arg	Thr	Phe	Pro	Leu	Leu	Asn	Lys	Val	Gly	
168		450				455						460					
170	gta	aac	aac	act	gtc	aca	acc	aca	gcc	gga	aat	gtc	att	tct	gtc	ata	2041
171	Val	Asn	Asn	Thr	Val	Thr	Thr	Thr	Ala	Gly	Asn	Val	Ile	Ser	Val	Ile	
172	465				470					475					480		
174	gga	agt	act	gaa	aca	aca	ggg	aaa	att	gtt	cca	agt	aca	aac	gga	att	2089
175	Gly	Ser	Thr	Glu	Thr	Thr	Gly	Lys	Ile	Val	Pro	Ser	Thr	Asn	Gly	Ile	
176				485					490					495			
178	tca	aat	gca	gaa	aac	agt	gtt	tcc	cag	cta	atc	tca	cgt	agt	act	gac	2137
179	Ser	Asn	Ala	Glu	Asn	Ser	Val	Ser	Gln	Leu	Ile	Ser	Arg	Ser	Thr	Asp	
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183	Ser	Thr	Leu	Arg	Ala	Leu	Glu	Thr	Val	Lys	Lys	Val	Gly	Lys	Val	Gly	
184			515					520					525				
186	gct	aat	ggt	cag	aat	gct	gct	ggg	ccc	tct	gca	gat	tct	gta	act	gaa	2233
187	Ala	Asn	Gly	Gln	Asn	Ala	Ala	Gly	Pro	Ser	Ala	Asp	Ser	Val	Thr	Glu	
188		530				535						540					
190	aat	aaa	att	ggt	tct	cca	ccc	aag	act	cct	gta	agt	aat	gta	gca	gct	2281
191	Asn	Lys	Ile	Gly	Ser	Pro	Pro	Lys	Thr	Pro	Val	Ser	Asn	Val	Ala	Ala	
192	545				550					555				560			
194	acc	tca	gct	ggg	ccc	tct	aat	gtt	gga	aca	gag	ctg	aat	tct	gtg	cct	2329
195	Thr	Ser	Ala	Gly	Pro	Ser	Asn	Val	Gly	Thr	Glu	Leu	Asn	Ser	Val	Pro	
196				565					570					575			
198	caa	aaa	tcc	agc	cca	ttt	cta	act	aga	gta	cca	gta	tat	cct	ccg	cat	2377
199	Gln	Lys	Ser	Ser	Pro	Phe	Leu	Thr	Arg	Val	Pro	Val	Tyr	Pro	Pro	His	

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204		595		600		605		
206	gaa gtc cca cag tac cca cag aca gga tac tat cca cca cct cca acg							2473
207	Glu Val Pro Gln Tyr Pro Gln Thr Gly Tyr Tyr Pro Pro Pro Pro Thr							
208		610		615		620		
210	gta cca gct ggt gtg gct ccc tgt gtt cct cgc ttt gtg agg tcc aat							2521
211	Val Pro Ala Gly Val Ala Pro Cys Val Pro Arg Phe Val Arg Ser Asn							
212	625		630		635		640	
214	aac gtt cca gag tcc tcc ctc cca cct gct tcc atg cca tat gcc gat							2569
215	Asn Val Pro Glu Ser Ser Leu Pro Pro Ala Ser Met Pro Tyr Ala Asp							
216		645		650		655		
218	cat tac agt aca ttt tcc cct cga gat cga atg aat tct tct cct tac							2617
219	His Tyr Ser Thr Phe Ser Pro Arg Asp Arg Met Asn Ser Ser Pro Tyr							
220		660		665		670		
222	cag cct cct cct ccg cag ccg tat gga cca gtt cct cca gta cct tct							2665
223	Gln Pro Pro Pro Pro Gln Pro Tyr Gly Pro Val Pro Pro Val Pro Ser							
224		675		680		685		
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230	atg tac caa cga gat gac att att aga agc aat tct tta cct cca atg							2761
231	Met Tyr Gln Arg Asp Asp Ile Ile Arg Ser Asn Ser Leu Pro Pro Met							
232	705		710		715		720	
234	gat gtg atg cac tca tct gtc tat cag aca tct ttg cgg gaa aga tat							2809
235	Asp Val Met His Ser Ser Val Tyr Gln Thr Ser Leu Arg Glu Arg Tyr							
236		725		730		735		
238	aac tca tta gat gga tat tat tcg gtg gct tgt cag cca cca agt gag							2857
239	Asn Ser Leu Asp Gly Tyr Tyr Ser Val Ala Cys Gln Pro Pro Ser Glu							
240		740		745		750		
242	cca agg aca act gtg cct tta cca agg gaa cct tgt ggt cat ttg aag							2905
243	Pro Arg Thr Thr Val Pro Leu Pro Arg Glu Pro Cys Gly His Leu Lys							
244		755		760		765		
246	acc agt tgc gag gag cag ata aga aga aag cca gat cag tgg gca cag							2953
247	Thr Ser Cys Glu Glu Gln Ile Arg Arg Lys Pro Asp Gln Trp Ala Gln							
248		770		775		780		
250	tac cac act cag aaa gca cct ctt gtc tct tca act ctt cct gtg gca							3001
251	Tyr His Thr Gln Lys Ala Pro Leu Val Ser Ser Thr Leu Pro Val Ala							
252	785		790		795		800	
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256		805		810		815		
258	gcg gat ttc tca gag agt gtg agt ggt aca aaa ttt gaa gaa gat cat							3097
259	Ala Asp Phe Ser Glu Ser Val Ser Gly Thr Lys Phe Glu Glu Asp His							
260		820		825		830		
262	ctt tcc cat tat tct ccc tgg tct tgt ggc acc ata ggc tcc tgt ata							3145
263	Leu Ser His Tyr Ser Pro Trp Ser Cys Gly Thr Ile Gly Ser Cys Ile							
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270	gtg tta atg gac ctg gac agt ggt gat gtt aag aga aga gta cat tta	3241
271	Val Leu Met Asp Leu Asp Ser Gly Asp Val Lys Arg Arg Val His Leu	
272	865 870 875 880	
274	ttt gaa acc cag aga agg aca aaa gaa gaa gat cca ata att ccc ttt	3289
275	Phe Glu Thr Gln Arg Arg Thr Lys Glu Glu Asp Pro Ile Ile Pro Phe	
276	885 890 895	
278	agt gat gga ccc atc atc tca aaa tgg ggt gcg att tcc aga tct tcc	3337
279	Ser Asp Gly Pro Ile Ile Ser Lys Trp Gly Ala Ile Ser Arg Ser Ser	
280	900 905 910	
282	cgt aca ggt tac cat acc aca gat cct gtc cag gcc act gct tcc caa	3385
283	Arg Thr Gly Tyr His Thr Thr Asp Pro Val Gln Ala Thr Ala Ser Gln	
284	915 920 925	
286	gga agt gcg act aag ccc atc agt gta tca gat tat gtc cct tat gtc	3433
287	Gly Ser Ala Thr Lys Pro Ile Ser Val Ser Asp Tyr Val Pro Tyr Val	
288	930 935 940	
290	aat gct gtt gat tca agg tgg agt tca tat ggc aac gag gcc aca tca	3481
291	Asn Ala Val Asp Ser Arg Trp Ser Ser Tyr Gly Asn Glu Ala Thr Ser	
292	945 950 955 960	
294	tca gca cac tat gtt gaa agg gac aga ttc att gtt act gat tta tct	3529
295	Ser Ala His Tyr Val Glu Arg Asp Arg Phe Ile Val Thr Asp Leu Ser	
296	965 970 975	
298	ggt cat aga aag cat tcc agt act ggg gac ctt ttg agc ctt gaa ctt	3577
299	Gly His Arg Lys His Ser Ser Thr Gly Asp Leu Leu Ser Leu Glu Leu	
300	980 985 990	
302	cag cag gcc aag agc aac tca tta ctt ctt cag aga gag gcc aat gct	3625
303	Gln Gln Ala Lys Ser Asn Ser Leu Leu Leu Gln Arg Glu Ala Asn Ala	
304	995 1000 1005	
306	ttg gcc atg caa cag aag tgg aat tcc ctg gat gaa ggc cgt cac	3670
307	Leu Ala Met Gln Gln Lys Trp Asn Ser Leu Asp Glu Gly Arg His	
308	1010 1015 1020	
310	ctt acc tta aac ctt tta agc aag gaa att gaa cta aga aat gga	3715
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314	gag tta cag agt gat tat aca gaa gat gca aca gat act aaa cct	3760
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316	1040 1045 1050	
318	gat agg gat atc gag tta gag ctt tca gca ctt gat act gat gaa	3805
319	Asp Arg Asp Ile Glu Leu Glu Leu Ser Ala Leu Asp Thr Asp Glu	
320	1055 1060 1065	
322	cct gat gga caa agt gaa cca att gaa gag atc ttg gac ata cag	3850
323	Pro Asp Gly Gln Ser Glu Pro Ile Glu Glu Ile Leu Asp Ile Gln	
324	1070 1075 1080	
326	ctt ggt atc agt tct caa aat gat cag ttg cta aat gga atg gca	3895
327	Leu Gly Ile Ser Ser Gln Asn Asp Gln Leu Leu Asn Gly Met Ala	
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